Full genome characterization of rotavirus A isolates from outbreaks of neonatal diarrhoea in pigs

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BACKGROUND

Rotavirus A (RVA) is one of the main causes of diarrhoea in pigs worldwide. Since the beginning of 2017, an apparent increase of outbreaks of neonatal diarrhoea associated with RVA was detected in Northern Spain. The outbreaks affected suckling pigs of all ages, including 1 to 7-day-old piglets and, in some farms, also sows, suggesting a lack of herd immunity against this virus.

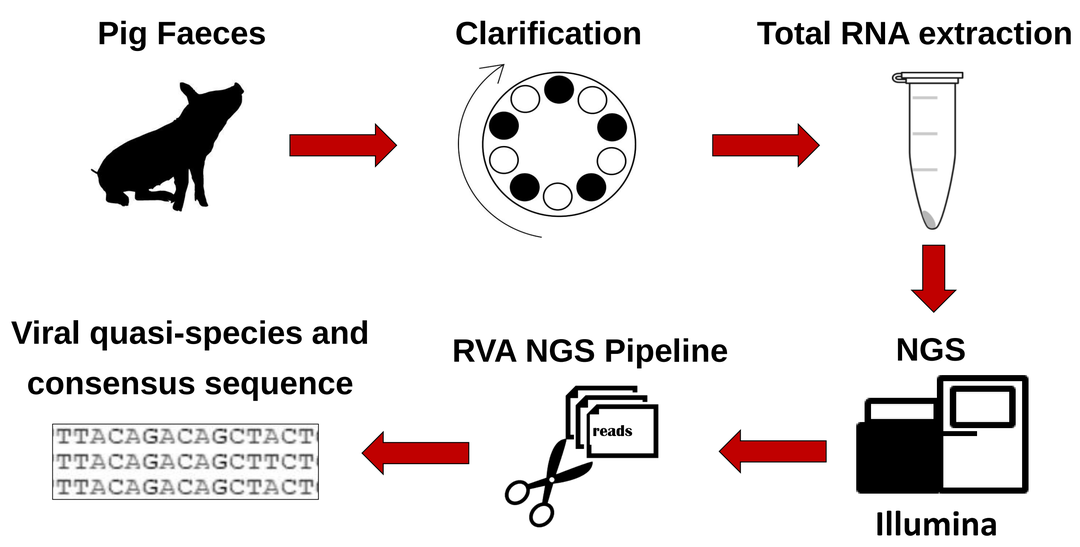
OBJECTIVES

1. Characterize the RVA involved in the outbreaks of neonatal diarrhoea in pigs and examine its possible genetic origin and evolution
2. Asses potential vaccine protection by determining the antigenic differences between the RVA isolates and the vaccine strains.

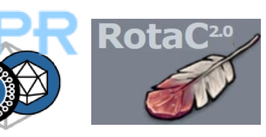
MATERIALS AND METHODS

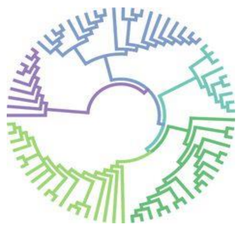
Samples had been collected from 16 apparently unrelated outbreaks of neonatal diarrhoea (< 7 days of age) in which RVA was detected as the sole infectious agent. Twenty-four faecal samples previously identified as RVA positive by RT-PCR were selected for further analysis.

NGS PROTOCOL



- Full genome genotyping of the RVA isolates.
- Phylogenetic analyses using animal and human RVA sequences available in GenBank.
- Bayesian estimations of the most recent common ancestor for VP1, VP6 and NSP5.
- Identification of RVA epitopes and comparison with porcine vaccine strains.





RESULTS

G and P genotypes were found to be highly diverse, while the diversity of the genome backbone was minimal. Two different genotype combinations were detected in 3 farms. G9P[23] was the most common.

	Farm	Sample	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5
C1	F1	253	G3	P[7]	I5	R1	C1	M1	A8	N1	T7	E1	H1
		255	G3	P[7]	I5	R1	C1	M1	A8	N1	T7	E1	H1
	F2	264	G4	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
		270	G4	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
	F3	284	G9	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
	F4	348	G9	P[23][a]	I5	R1	C1	M1	A8	N1	T7	E1	H1
C2	F5	222	G9	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
	F6	341	G9	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
	F7	437	G3	P[19]	I5	R1	C1	M1	A8	N1	T7	E1	H1
		438	G5	P[19]	I5	R1	C1	M1	A8	N1	T7	E9	H1
C3	F8	447	G9	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
		448	G9	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
	F9	451	G9	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
		452	G9	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
C4	F10	376	G4	P[7]	I5	R1	C1	M1	A8	N1	T7	E1	H1
	F11	393	G9	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
		394	G9	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
C5	F12	35	G9	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
		37	G3	P[7]	I5	R1	C1	M1	A8	N1	T7	E1	H1
C6	F13	471	G3	P[13]	I5	R1	C1	M1	A8	N1	T7	E1	H1
		473	G9	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
C7	F14	108	G9	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1
C8	F15	456	G5	P[13]	I5	R1	C1	M1	A8	N1	T7	E1	H1
C9	F16	486	G9	P[23]	I5	R1	C1	M1	A8	N1	T7	E1	H1

Figure 1. Full genome genotypes of the RVA sequenced in this study. [a]: Two P genotypes were found; P[23] and P[28].

All isolates had a common ancestor probably introduced between March and May 2016 and were possibly of pig origin.

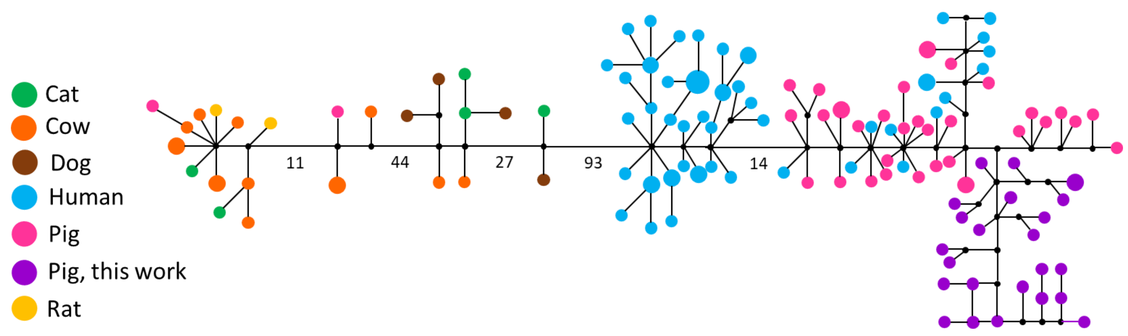


Figure 2. Median-joining network based on the amino acid sequences of the VP1 gene using animal and human sequences available in GenBank

High antigenic differences between the RVA isolates and the vaccine strains were determined.

CONCLUSIONS

- ✓ Novel RVA strains may disseminate rapidly in the population and undergo an extremely high diversification in a very short period of time.
- ✓ Development of vaccines for new types of RVA could be useful for further control of this infection.